AMENDMENTS TO THE CLAIMS

1-5 (canceled).

6 (currently amended) A method for detecting the presence of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a sample, comprising:

a) providing:

(i) a sample; and

(ii) cells chosen from human embryonic kidney (HEK)-293, HEK-293T, Huh-7, Mv1Lu, Mv1Lu-hf and ~~pRHMK~~ primary rhesus monkey kidney (pRHMK) cells;

b) inoculating said cells with said sample to produce inoculated cells; and

c) detecting the presence of said SARS-coronavirus in said inoculated cells, wherein said detecting comprises detecting the presence of SARS-coronavirus subgenomic RNA.

7 (canceled).

8 (previously presented) The method of Claim 6, wherein said detecting further comprises detecting the presence of SARS-coronavirus genomic RNA.

9 (previously presented) The method of Claim 6, wherein said detecting further comprises detecting the presence of a SARS-coronavirus polypeptide.

10 (currently amended) The method of Claim 6, wherein said cells comprise ~~a transgenic cell~~ HEK-293 cells.

11 (canceled).

12 (currently amended) The method of Claim 6, wherein said cells comprise ~~a wild-type cell~~ HEK-293T cells.

13 (original) The method of Claim 6, wherein said cells are in single cell type culture.

14 (original) The method of Claim 6, wherein said cells are in mixed cell type culture with a second cell type.

15 (canceled).

16 (original) The method of Claim 6, wherein said sample is isolated from a mammal.

17 (original) The method of Claim 6, wherein said mammal is human.

18 (currently amended) A method for detecting the presence of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a first sample and in a second sample, comprising:

a) providing:

(i) a first sample;

(ii) a second sample;

b) contacting test cells chosen from human embryonic kidney (HEK)-293, HEK-293T, Huh-7, Mv1Lu, Mv1Lu-hf and ~~pRHMK~~ primary rhesus monkey kidney (pRHMK) cells with:

(i) said first sample to produce a first treated sample; and

(ii) said second sample to produce a second treated sample;

wherein said contacting is such that said test cells are infected with SARS-coronavirus if present in one or both of said first sample and said second sample;

c) detecting the presence of one or both of SARS-coronavirus genomic RNA and SARS-coronavirus subgenomic RNA in said first treated sample and said second treated sample, wherein said detecting indicates the presence of said SARS-coronavirus in one or both of said first treated sample and said second treated sample.

19 (original) The method of Claim 18, wherein said detecting comprises detecting an absence of SARS-coronavirus subgenomic RNA in said first treated sample.

20 (original) The method of Claim 18, wherein said detecting comprises detecting a reduced level of SARS-coronavirus subgenomic RNA in said first treated sample compared to the level of subgenomic RNA in said second treated sample.

21 (original) The method of Claim 18, wherein said detecting comprises detecting a reduced ratio of SARS-coronavirus subgenomic RNA level to SARS-coronavirus genomic RNA level in said first treated sample compared to said ratio in said second treated sample.

22 (original) The method of Claim 18, wherein said first sample and said second sample are isolated from a mammal.

23 (original) The method of Claim 18, wherein said mammal is human.

24 (currently amended) A method for identifying a test agent as altering replication of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a cell, comprising:

a) providing cells ~~treated with a first test agent, wherein said cells are~~ chosen from human embryonic kidney (HEK)-293, HEK-293T, Huh-7, Mv1Lu, Mv1Lu-hf ~~and pRHMK;~~ and primary rhesus monkey kidney (pRHMK) cells;

b) treating said cells with a sample comprising SARS-coronavirus before or after incubating said cells in the presence and absence of a first test agent; and

c) detecting an altered level of replication of SARS-coronavirus in cells treated with said first test agent compared to a level of replication of SARS-coronavirus in cells not treated with said first test agent, wherein said detecting identifies said first test agent as altering replication of SARS-coronavirus in a cell, and said detecting comprises detecting SARS-coronavirus subgenomic RNA in one or both of said cells treated with a first test agent and said cells not treated with said first test agent.

25 (original) The method of Claim 24, wherein said altered level is a reduced level.

26 (original) The method of Claim 24, wherein said altered level is an increased level.

27 (canceled).

28 (previously presented) The method of Claim 24, wherein said detecting further comprises detecting SARS-coronavirus genomic RNA.

29 (previously presented) The method of Claim 24, wherein said detecting further comprises detecting SARS-coronavirus polypeptide.

30 (original) The method of Claim 24, further comprising detecting SARS-coronavirus particles.

31 (previously presented) The method of Claim 24, wherein said detecting further comprises detecting an absence of SARS-coronavirus genomic RNA in said cells treated with said first test agent.

32 (original) The method of Claim 24, wherein said detecting comprises detecting a reduced level of SARS-coronavirus subgenomic RNA in said cells treated with said first test agent compared to the level of SARS-coronavirus subgenomic RNA in said cells that are not treated with said first test agent.

33 (currently amended) The method of Claim 32, wherein detecting an increased reduction in the level of SARS-coronavirus subgenomic RNA in said cells treated with said first test agent compared to said cells treated with ~~said second~~ a second test agent identifies said first test agent as more efficacious than said second test agent in reducing replication of SARS-coronavirus in a cell.

34 (original) The method of Claim 24, wherein said detecting comprises detecting a reduced ratio of SARS-coronavirus subgenomic RNA level relative to SARS-coronavirus genomic RNA level in said cells treated with said first test agent compared to said ratio in said cells that are not treated with said first test agent.

35 (currently amended) The method of Claim 34, wherein detecting an increased reduction in said ratio of SARS-coronavirus subgenomic RNA level to SARS-coronavirus genomic RNA level in said cells treated with said first test agent compared to said ratio in said cells treated with ~~said second~~ a second test agent identifies said first test agent as more efficacious than said second test agent in reducing replication of SARS-coronavirus in a cell.

36-47 (canceled).

48 (new) The method of Claim 6, wherein said cells comprise Huh-7 cells.

49 (new) The method of Claim 6, wherein said cells comprise Mv1Lu cells.

50 (new) The method of Claim 6, wherein said cells comprise Mv1Lu-hF cells.

51 (new) The method of Claim 6, wherein said cells comprise pRHMK cells.